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SEQUENCE LISTING

<110> UNIVERSITY COLLEGE LONDON

<120> SCREEN METHOD

<130> N75751B

<140> PCT/GB00/00226
<141> 2000-01-26

<150> GB 9901705.5
<151> 1999-01-26

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<151> 1999-06-04

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 858

<212> DNA

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<221> CDS

<222> (1)..(858)

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 Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
 1 5 10 15

gtg gtg ccg gcg cta ccc gag tcg ctc tgc cag cac gcg ctg aga arg 96
 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
 20 25 30

gcc aag ggc gag gag gtg gac gtc gcc cgc gcg gaa cgg cag cac cac cag 144
 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
 35 40 45

ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag 192
 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gin Val Val Glu
 50 55 60

ctg ccg gcc gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg 240
 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
 65 70 75 80

gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg gcg ccg 288
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
 85 90 95

agc'cg	agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt	336
Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu		
100	105	110
cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc	384	
Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly		
115	120	125
gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa	432	
Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys		
130	135	140
agg aca aat caa cga ggt gct gaa atc ttg gct gat act ttt aag gac	480	
Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp		
145	150	155
160		
tat gca gtc tcc aca gtg cca gtg gca gat ggg ttg cat ttg aag agt	528	
Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser		
165	170	175
tcc tgc agc atg gct ggg cct aac ctg atc gca att ggg tct agt gaa	576	
Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu		
180	185	190
tct gca cag aag gcc ctt aag atc atg caa cag atg agt gac cac cgc	624	
Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg		
195	200	205
taa gac aaa ctc act gtg cct gat gac ata gca gca aac tgt ata tat	672	
Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr		
210	215	220
cta aat atc ccc aac aaa ggg cac gtc ttg ctg cac cga acc ccg gaa	720	
Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu		
225	230	235
240		
gag tat cca gaa agt gca aag gtt tat gag aaa ctg aag gac cat atg	768	
Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met		
245	250	255
ctg atc ccc gtg agc atg tct gaa ctg gaa aag gtg gat ggg ctg ctc	816	
Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu		
260	265	270
acc tgc tgc tca gtt tta att aac aag aag gta gac tcc tga	858	
Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser		
275	280	285

<210> 2

<211> 285

<212> PRT

<213> H. Sapiens

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Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gin His Ala Leu Arg Ser
20 25 30

Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
35 40 45

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gin Val Val Glu
50 55 60

Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
65 70 75 80

Ala Val-Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
85 90 95

Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
100 105 110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
130 135 140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
145 150 155 160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
165 170 175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
210 215 220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
245 250 255

Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
260 265 270

Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
275 280 285

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<222> (1)..(858)

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1 5 10 15

cgg gga gtc cca gag agc ctg gcg tcg ggg gaa ggt gct ggc 96
Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
20 25 30

ctt ccc gct ctg gat ctg gcc aaa gct caa agg gag cac ggg gtg ctg 144
Leu Pro Ala Leu Asp Leu Ala Lys Ala Gin Arg Glu His Gly Val Leu
35 40 45

gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca 192
Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gin Leu Leu Glu Leu Pro
50 55 60

cct gag gag tca ttg ccg ctg gga ccg ctg ctt ggc gac acg gcc gtg 240
Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
65 70 75 80

atc caa ggg gac acg gcc cta atc acg cgg ccc tgg agc ccc gct cgt 288
Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
85 90 95

agg cca gag gtc gat gga gtc cgc aaa gcc ctg caa gac ctg ggg ctc 336
Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
100 105 110

cga att gtg gaa ata gga gac aac gcg acg ctg gat ggc act gac 384
Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
115 120 125

gtt ctc ttc acc ggc ccg gag ttt ttc gta ggc ctc tcc aaa tgg acc 432
Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
130 135 140

aat cac cga gga gct gag atc gtg gcg gac acg ttc cgg gac ttc gcc 480
Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
145 150 155 160

gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc 528
Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
165 170 175

ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc 576

Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
180 185 190

caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc 624
Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
195 200 205

tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt 672
Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg
210 215 220

cct ggg ttg cct ggt gtg ccc cct ttc ctc ctg cac cgt gga ggt ggg 720
Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
225 230 235 240

gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc 768
Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
245 250 255

ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc 816
Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
260 265 270

agc tcc ctc tgc ttg gtg ctc agc aca cgc ccc cac agc tga 858
Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
275 280 285

<210> 4
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<212> PRT
<213> H. sapiens

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Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
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Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
20 25 30

Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
35 40 45

Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
50 55 60

Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
65 70 75 80

Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
85 90 95

Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
100 105 110

Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
115 120 125

Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
130 135 140

Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
145 150 155 160

Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
165 170 175

Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
180 185 190

Gln Lys-Ala Val Arg Ala-Met Ala Val Leu Thr Asp His Pro Tyr Ala
195 200 205

Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg
210 215 220

Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
225 230 235 240

Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
245 250 255

Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
260 265 270

Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
275 280 285

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<211> 777

<212> DNA

<213> S. coelicolor

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<221> CDS

<222> (1)..(777)

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1 5 10 15

gaa gga ctg gtg aca cac gtc gag cgg gag cag gtc gat cac ggc ctg 96
Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
20 25 30

gcc ctc gaa cag tgg gac gcc tac gtc gag gcc ctc gga gca cac ggc 144
Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly

35	40	45	
tgg gag act ctg gag gtg gac ccg gcc gag tac tgt ccg gac tcc gtc Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val	50	55	60
ttc gtc gag gac gcc gtc gtg ttc cgc aac gtc gcg ctg atc acg Phe Val Glu Asp Ala Val Val Phe Arg Asn Val Ala Leu Ile Thr	65	70	75
cgg ccc ggc gcc gag tcg cgg cgc ggc gag acg gcc ggc gtc gag gag Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu	85	90	95
gcc gtg gcc cgg ctc ggc tgc tcg gtg aac tgg gtg tgg gag ccg ggc Ala Val-Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Pro Gly	100	105	110
acc ctg gac ggc ggc gac gtc ctg aag atc ggc gac acg atc tac gtg Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val	115	120	125
gga cgc ggc ggc cgg acc aac gcg gcc ggt gtc cag cag ttg cgg cgc Gly Arg Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala	130	135	140
gcg ttc gag cgg ctg ggc gcc cgg gtc gtc gcc gtg ccc gtg agc aag Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys	145	150	155
gtg ctg cat ctg aag tcg cgg gtc acc gcg ctg cgg gac ggg acg gtg Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val	165	170	175
atc ggg cac atc ccc ctg acg gac gtg ccc tcg ctg ttc ccc cgt ttc Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe	180	185	190
ctg ccc gtg ccc gag gag tcg ggg ggc cac gtg gtg ctg ctc ggc ggg Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly	195	200	205
agc agg ctg ctg atg gcg gcg agc gcg ccc aag acg gcg gag ctg ctc Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu	210	215	220
gcc gat ctc ggt cac gag ccg gtg ctc gtc gac atc ggg gag ttc gag Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu	225	230	240
aag ctg gag ggc tgt gtg acg tgc ctc tcg gtc agg ctg cgc gag ctg Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu	245	250	255
tac gac tga			777

Tyr Asp

<210> 6

<211> 258

<212> PRT

<213> S. coelicolor

<400> 6

Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala
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Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
20 25 30

Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
35 40 45

Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val
50 55 60

Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr
65 70 75 80

Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu
85 90 95

Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly
100 105 110

Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val
115 120 125

Gly Arg Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala
130 135 140

Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys
145 150 155 160

Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val
165 170 175

Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe
180 185 190

Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly
195 200 205

Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu
210 215 220

Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu
225 230 235 240

Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu

245

250

255

Tyr Asp

<210> 7
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<213> P. aeruginosa

<220>
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<222> (1)..(765)

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ggc ctg acc tcc agc cac ctc ggc aag ccg gac tac gcc aag gcc ctg 96
Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu
20 25 30

gag cag cac aac gcc tac atc cgc gcc ttg cag acc tgc gac gtg gac 144
Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
35 40 45

atc acc ctg ctg ccg ccg gac gaa cgc ttc ccc gac tcg gtg ttc gtc 192
Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
50 55 60

gag gac ccg gtg ctc tgc acc tcg cgc tgc gcc atc atc acc cgc ccc 240
Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro
65 70 75 80

ggc gcc gaa tcg ccg cgc ggc gag acc gag atc atc gag gaa acc gtg 288
Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val
85 90 95

cag cgc ttc tat ccg ggc aag gtc gag cgc atc gag gca ccc ggc acg 336
Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
100 105 110

gtg gaa gcc ggc gac atc atg atg gtc ggc gac cac ttc tac atc ggc 384
Val Glu Ala Gly Asp Ile Met Met Val Glu Asp His Phe Tyr Ile Gly
115 120 125

gaa tcg gcc cgc acc aac gcc gag ggc gcc ccg cag atg atc gcg atc 432
Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
130 135 140

ctg gag aaa cat ggc ctc agc ggc tcg gtg gtg cgc ctg gaa aag gtc 480
Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
145 150 155 160

ctg cac ctg aag acc ggg ctc gcc tac ctg gaa cac aac aac ctg ctg 528
Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu
165 170 175

gcc gcc ggc gag ttc gtc agc aag ccg gag ttc cag gac ttc aac atc 576
Ala Ala Gly Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile
180 185 190

atc gag atc ccc gaa gag gag tcc tac gcc aac tgc atc tgg gtc 624
Ile Glu Ile Pro Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
195 200 205

aac gaa agg gtg atc atg ccc gcc ggc tat ccc cgg acc cgc gag aag 672
Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys
210 215 220

atc gcc cgc ctc ggc tac cgg gtg atc gag gtg gac acc tcc gaa tat 720
Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr
225 230 235 240

cgc aag atc gac ggc ggc gtc agt tgc atg tcg ctg cgc ttc tga 765
Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe
245 250 255

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<212> PRT
<213> *P. aeruginosa*

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20 25 30

Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
35 40 45

Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
50 55 60

Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro
65 70 75 80

Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val
85 90 95

Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
100 105 110

Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
115 120 125

Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
130 135 140

Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
145 150 155 160

Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu
165 170 175

Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile
180 185 190

Ile Glu Ile Pro Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
195 200 205

Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys
210 215 220

Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr
225 230 235 240

Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe
245 250

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<211> 1257
<212> DNA
<213> *P. aeruginosa*

<220>
<221> CDS
<222> (1)..(1257)

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ctg cgc aaa gtg atg gtc tgc tcg ccc gga ctc gcc cac cag cgc ctg 96
Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
20 25 30

acc ccg agc aac tgc gac gag ttg ctg ttc gac gac gtg atc tgg gtg 144
Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
35 40 45

aac cag gcc aag cgc gac cac ttc gac ttc gtc acc aag atg cgc gag 192
Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
50 55 60

cgc ggc atc gac gtc ctc gag atg cac aat ctg ctg acc gag acc atc 240
Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
65 70 75 80

cag aac ccg gaa gcg ctg aag tgg atc ctc gat cgc aag atc acc gcc Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala	288
85 90 95	
gac agc gtc ggc ctg ggc ctg acc agc gag ctg cgc tcc tgg ctg gag Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu	336
100 105 110	
agc ctg gag ccg cgc aag ctg gag tac ctg atc ggc ggc gtc gcc Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Val Ala	384
115 120 125	
gct gac gac ctg ccc gcc agc gaa ggc gcc aac atc ctc aag atg tac Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr	432
130 135 140	
cgc gag tac ctg ggc cat tcc agc ttc ctg ctg cgc ttc cgc aac Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn	480
145 150 155 160	
acc cag ttc acc ccg gac acc act tgc tgg atc tac ggc ggc gtg acc Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr	528
165 170 175	
ctg aac ccg atg tac tgg ccg gcg cga cga cag gaa acc ctg ctg acc Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr	576
180 185 190	
acc gcc atc tac aag ttc cac ccc gag ttc gcc aac gcc gag ttc gag Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu	624
195 200 205	
atc tgg tac ggc gac ccg gac aag gac cac gcc tcc tgg acc ctg gaa Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu	672
210 215 220	
ggc ggc gac gtg atg ccg atc ggc aac ggc gtg gtc ctg atc ggc atg Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met	720
225 230 235 240	
ggc gag ccg tcc tgg ccg cag gcc atc ggt cag gtc gcc cag tgg ctg Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu	768
245 250 255	
ttc gcc aag ggc gcc ggc gag ccg gtg atc gtc gcc ggc ctg ccg aag Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys	816
260 265 270	
tcc ccg gcc gcg atg cac ctg gac acc gtg ttc agc ttc tgc gac cgc Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg	864
275 280 285	
gac ctg gtc acg gtc ttc ccg gaa gtg gtc aag gaa atc gtg ccc ttc Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe	912
290 295 300	

agc ctg cgc ccc gat ccg agc agc ccc tac ggc atg aac atc cgc cgc 960
Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
305 310 315 320

gag gag aaa acc ttc ctc gaa gtg gtc gcc gaa tcc ctc gcc ctg aag 1008
Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys
325 330 335

aaa ctg cgc gtg gtc gag acc ggc ggc aac agc ttc gcc gcc gag cgc 1056
Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
340 345 350

gag caa tgg gac gac ggt aac aac gtg gtc tgc ctg gag ccg ggc gtg 1104
Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
355 360 365

gtg gtc ggc tac gac cgc aac acc tac acc aac acc ctg ctg cgc aag 1152
Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
370 375 380

gcc ggc gtc gag gtc atc acc acc agc gcc agc gaa ctg ggt cgc ggt 1200
Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly
385 390 395 400

cgc ggc ggc cac tgc atg acc tgc ccg atc gtc cgc gac ccg atc 1248
Arg Gly Gly Gly His Met Thr Cys Pro Ile Val Arg Asp Pro Ile
405 410 415

gac tac tga 1257
Asp Tyr

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<212> PRT
<213> P. aeruginosa

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Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
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Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
35 40 45

Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
50 55 60

Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
65 70 75 80

Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala
85 90 95

Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
100 105 110

Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala
115 120 125

Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr
130 135 140

Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn
145 150 155 160

Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
165 170 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
180 185 190

Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
195 200 205

Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu
210 215 220

Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met
225 230 235 240

Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu
245 250 255

Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys
260 265 270

Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
275 280 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe
290 295 300

Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
305 310 315 320

Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys
325 330 335

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
340 345 350

Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
355 360 365

Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
370 375 380

Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly

385 390 395 400

Arg Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile
405 410 415

Asp Tyr

<210> 11

<211> 1014

<212> DNA

<213> M. tuberculosis

<220>

<221> CDS

<222> (69)..(986)

<400> 11

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gttggttt atg acg gat tcc tac gtc gct gct gtc cgt cta ggg tca cct 110
Met Thr Asp Ser Tyr Val Ala Ala Ala Arg Leu Gly Ser Pro
1 5 10

gca cgc cgc acc ccc cgg acg cgg tat gca atg acc ccg cgg gcc 158
Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala
15 20 25 30

tcc ttt gcc gtc gca tac gcg atc aac ccc tgg atg gag gtc acc gcg 206
Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala
35 40 45

cca gtc gac gtc caa gtc gcg caa gca cag tgg gag cac ctc cac cag 254
Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln
50 55 60

acc tat ctt cgg cta ggc cac agc gtg gat ctg atc gag ccc att tcc 302
Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser
65 70 75

ggg tta ccg gac atg gtg tac acc gcc aac ggt ggg ttc atc gcg cac 350
Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His
80 85 90

gac atc gcc gtg gtc gcc cgg ttc cgg ttc ccc gaa cga gct ggt gag 398
Asp Ile Ala Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu
95 100 105 110

tct aga gcc tat gcc agc tgg atg tcc tcg gtc gga tat cgc ccg gtg 446
Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val
115 120 125

acc acc cgc cac gtc aac gag gga cag ggc gac ctg ctg atg gtt ggc 494
Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly

130

135

140

gaa agg gtg ttg gcg ggc tac ggc ttt cgc aca gac cag cgc gca cac 542
Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His
145 150 155

gcc gaa atc gcc gcg gtg ctt ggt ctg ccg gtg gtc tcc ctc gag ttg 590
Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu
160 165 170

gtc gac cca cgg ttc tat cac ctg gac acc gcg ctg gcc gtg ctc gac 638
Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp
175 180 185

gac cac acg atc gcc tac tac ccg ccg gtc agt acg gca gcg cag 686
Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln
195 200 205

gaa cag ttg tcg gcg ctg ttc ccc gac gcg att gtg gtc ggc agt gcc 734
Glu Gin Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala
210 215 220

gac gcg ttc gtg ttc gga ctc aac gcc gtc tct gac ggt ctg aac gta 782
Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val
225 230 235

gtg ctt ccg gtc gcg gcc atg ggt ttt gcg gcg cag tta cgc gca gcc 830
Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala Gin Leu Arg Ala Ala
240 245 250

ggc ttc gag ccg ggt gtc gat ctg tcc gag ctg ctc aag ggc ggc 878
Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly
255 260 265 270

ggt tcc gtc aag tgc tgc acg ctg gag ata cac cca tga caa atc tcg 926
Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His Pro Gin Ile Ser
275 280 285

cgg atg cca ctc agg cca cta tgg cac tgg tcg aaa ggc atg cag cgc 974
Arg Met Pro Leu Arg Pro Leu Trp His Trp Ser Lys Gly Met Gln Arg
290 295 300

aca att att cgc cgctgcctgt ggtggcgccc agcgcgtga 1014
Thr Ile Ile Arg
305

<210> 12

<211> 282

<212> PRT

<213> M. tuberculosis

<400> 12

Met Thr Asp Ser Tyr Val Ala Ala Ala Arg Leu Gly Ser Pro Ala Arg

1 5 10 15

Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala Phe Phe
20 25 30

Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala Pro Val
35 40 45

Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln Thr Tyr
50 55 60

Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser Gly Leu
65 70 75 80

Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His Asp Ile
85 90 95

Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu Ser Arg
100 105 110

Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val Thr Thr
115 120 125

Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly Glu Arg
130 135 140

Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His Ala Glu
145 150 155 160

Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu Val Asp
165 170 175

Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp Asp His
180 185 190

Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln Glu Gln
195 200 205

Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala Asp Ala
210 215 220

Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val Val Leu
225 230 235 240

Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala Gly Phe
245 250 255

Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly Gly Ser
260 265 270

Val Lys Cys Cys Thr Leu Glu Ile His Pro
275 280

<210> 13
<211> 305
<212> PRT

<213> M. tuberculosis

<400> 13

Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile
1 5 10 15

Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala
20 25 30

Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala
35 40 45

Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp
50 55 60

Met Asp Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp
65 70 75 80

Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu
85 90 95

Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu

275

280

285

Leu Leu Lys Gly Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His
290 295 300

Pro
305

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(1) APPLICANT:

(A) NAME: UNIVERSITY COLLEGE LONDON
(B) STREET: Gower Street
(C) CITY: London
(E) COUNTRY: United Kingdom
(F) POSTAL CODE (ZIP): WC1E 6BT

(11) TITLE OF INVENTION: SCREEN METHOD

(111) NUMBER OF SEQUENCES: 12

(1v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(1i) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGCCCGGCC TCGGCCACCC CTCCGCTTC GGCGGGCCA CCCACGGGT GGTGGGGCG	60
CTACCCGAGT CGCTCTGCCA GCACGGCTG AGAACGCCA AGGGCGAGGA GGTGGACGTC	120
GCCCCGGCGG AACGGCAGCA CCAGCTCTAC GTGGGGTGC TGCGCAGCAA GCTGGGCTG	180
CAGGTGGTGG AGCTGCCGGC CGACGAGAGC CTTCCGGACT GCGTCTTGTG GGAGGACGTG	240
GCCGTGGTGT GCGAGGAGAC GGCCTCTAC ACCCGACCCG GGGCGCGAG CGGGAGGAAG	300
GAGGTTGACA TGATGAAAGA ACCATTAGAA AAACTTCAGC TCAATATACT AGAGATGAAA	360
GATGAAAATG CAACTTCTAGA TGGCGGAGAT GTTTTATTCA CAGGCAGAGA ATTTTTGTG	420
GGCTTTCCA AAAGGACAAA TCAACGAGGT GCTGAAATCT TGGCTGATAC TTTTAAGGAC	480

TATGCAGTCT CCACAGTGCC AGTGGCAGAT GGGTTGCATT TGAAGAGTTT CTGCAGCATG	540
GCTGGGCCCTA ACCTGATCGC AATTGGGTCT AGTGAATCTG CACAGAAGGC CCTTAAGATC	600
ATGCAACAGA TGAGTGACCA CGCTACGAC AAACACTACTG TGCTGTATGA CATAGCAGCA	660
AACTGTATAT ATCTAAATAT CCCCAACAAA GGGCACGTCT TGCTGCACCG AACCCCGGAA	720
GAGTATCCAG AAAGTGCAA GGTTTATGAG AAACGTGAAGG ACCATATGCT GATCCCCGTG	780
AGCATGTCCTG AACTGGAAAA GGTGGATGGG CTGCTCACCT GCTGCTCAGT TTAAATTAAC	840
AAGAAGGTTAG ACTCCTGA	858

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala			
1	5	10	15
Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser			
20	25	30	
Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln			
35	40	45	
Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu			
50	55	60	
Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val			
65	70	75	80
Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro			
85	90	95	
Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu			
100	105	110	
Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly			
115	120	125	

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Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 130 135 140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
 145 150 155 160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
 165 170 175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
 180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
 195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
 210 215 220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
 225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
 245 250 255

Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
 260 265 270

Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGGGACGC CGGGGGAGGG GCTGGGCCGC TGCCTCCATG CCCTGATCCG GGGAGTCCCA	60
GAGAGCCTGG CGTCGGGGGA AGGTGGGGGG GCTGGCCTTC CCCTCTGGA TCTGGCCAAA	120
GCTCAAAGGG AGCACGGGGT GCTGGGAGGT AAACCTGAGGC AACGACTGGG GCTACAGCTG	180
CTAGAACTGC CACCTGAGGA GTCAATTGCCG CTGGGACCGC TGCTTGCGGA CAOGGCCGTG	240
ATCCAAGGGG ACACGGCCCT AATCACGCGG CCCTGAGGCC CCGCTCGTAG GCCAGAGGTC	300

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GATGGAGTCC GCAAAGCCT GCAAGACCTG GGCGTCCGAA TTGTGGAAT AGGAGACGAG	360
AACGGGACCC TGGATGGCAC TGACGTTCTC TTCACCGGCC GGGAGTTTT CGTAGGCCTC	420
TCCAAATGGA CCAATCACCG AGGAGCTGAG ATCGTGGCGG ACACGTTCCG GGACTTCGCC	480
GTCTCCACTG TGCCAGTCTC GGGTCCCTCC CACCTGCGCG GTCTCTGCGG CATGGGGGA	540
CCTCGCACTG TTGTGGCAGG CAGCAACGAC GCTGCCAAA AGGCTGTCGS GGCAATGGCA	600
GTGCTGACAG ATCACCCATA TGCCCTCCCTG ACCCTCCAG ATGACCGAGC TGCTGACTGT	660
CTCTTTCTTC GTOCTGGTT GCCTGGTGTG CCCTTTTCC TCCTGCACCG TGGAGGTGGG	720
GATCTGCCCA ACAGCCAGGA GGCACTGCAG AAGCTCTCTG ATGTCACCCCT GGTAACCTGTG	780
TCTTGCTCAG AACTGGAGAA AGCTGGCGCC GGACTCAGCT CCCTCTGCTT GGTGCTCAGC	840
ACACGGCCCC ACAGCTGA	868

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile
 1 5 10 15

Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
 20 25 30

Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
 35 40 45

Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
 50 55 60

Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
 65 70 75 80

Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
 85 90 95

Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu

-5-

100

105

110

Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
115 120 125

Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
130 135 140

Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
145 150 155 160

Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
165 170 175

Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala
180 185 190

Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
195 200 205

Ser Leu Thr Leu Pro Asp Asp Ala Ala Asp Cys Leu Phe Leu Arg
210 215 220

Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
225 230 235 240

Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
245 250 255

Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu
260 265 270

Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO: 5:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GTGCCAGCA AGAAGGCCT GGTCCGCCGC CCCAGCCCCA GGCTCGCCGA AGGACTGGTG 60

ACACACGTGG	AGCGGGAGCA	GGTCGATCAC	GGCCTGGGCC	TGAAACAGTG	GGACGCCTAC	120
GTCGAGGCC	CTGGAGCACA	CGGCTGGGAG	ACTCTGGAGG	TGGACCCGGC	CGAGTACTGT	180
CGGACTCGG	TCTTCGTCGA	GGACGCCGTC	GTCGTTTCC	GCAACGTGCG	GCTGATCACG	240
CGGCCCCGG	CGAGTCGCG	CGCGCGGGAG	ACGGCCGGCG	TGAGGGAGSC	CSTGGCCCGG	300
CTCGGCTGCT	CGGTGAAC TG	GGTGTGGGAG	CCGGGCACCC	TGGACGGCGG	CGACGTCTCG	360
AAGATCGCG	ACACGATCTA	CGTGGGACGC	GGGGCCGGA	CCAACGCGGC	CGGTGTGACAG	420
CAGTTGCGG	CGGGCGTTGGA	GCCGCTGGGC	GCCCGGGTCC	TGCGCGTCCC	CGTGACGCAAG	480
GTGCTGCATC	TGAAGTCGGC	GGTCACCGCG	CTGCGGAGG	GGACGGTGAT	CGGGCACATC	540
CGGCTGACGG	ACGTGCGCTC	GCTGTTCCCG	CGTTTCCCTGC	CGGYGCGCGA	GGAGSTGGGG	600
GGCACGTTGG	TGCTGCTCGG	CGGGAGCAGG	CTGCTGATGG	CGGGCAGCGC	GCCCAAGACG	660
GCGGAGCTGC	TGCGCGATCT	CGGTACCGAG	CCGGTGTGCG	TGACATCGG	GGAGTTGAG	720
AAGCTGGAGG	GCTGTGTGAC	GTGCGCTCTCG	GTCAGGCTGCG	GCGAGCTGTA	CGACTGAG	777

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Val	Pro	Ser	Lys	Lys	Ala	Leu	Val	Arg	Arg	Pro	Ser	Pro	Arg	Leu	Ala	
1							5							10		15
Glu	Gly	Leu	Val	Thr	His	Val	Glu	Arg	Glu	Gln	Val	Asp	His	Gly	Leu	
							20							25		30
Ala	Leu	Glu	Gln	Trp	Asp	Ala	Tyr	Val	Glu	Ala	Leu	Gly	Ala	His	Gly	
							35							40		45
Trp	Glu	Thr	Leu	Glu	Val	Asp	Pro	Ala	Glu	Tyr	Cys	Pro	Asp	Ser	Val	
							50							55		60
Phe	Val	Glu	Asp	Ala	Val	Val	Val	Phe	Arg	Asn	Val	Ala	Leu	Ile	Thr	

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65 70 75 80
Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu
85 90 95
Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly
100 105 110
Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val
115 120 125
Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gin Gin Leu Arg Ala
130 135 140
Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys
145 150 155 160
Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val
165 170 175
Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe
180 185 190
Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly
195 200 205
Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu
210 215 220
Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu
225 230 235 240
Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu
245 250 255
Tyr Asp

(2) INFORMATION FOR SEQ ID NO: 7:

(f) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGTTCAAGC ACATCATCGC TCGCACGCC GCGCGCAGCC TGGTCGACGG CCTGACCTCC 60

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AGCCACCTCG	CAAGCCGGA	CTACGCCAAG	GCCCTGGAGC	AGCACAAACGC	CTACATCCGC	120
GCCTTGCAGA	CCTGGGACGT	GGACATCACC	CTGCTGCCGC	CGGACGAACG	CTTCCCCSAC	180
TGGTGTTCG	TCGAGGACCC	GGTGCTCTGC	ACCTGGCGCT	GCGCCATCAT	CACCCGGCCC	240
GGGCCGAAT	CCGGCGCGG	CGAGACCGAG	ATCATCGAGG	AAACCGTGCA	GCGTTCTAT	300
CCGGCAAGG	TCGAGGCAT	CGAGGCACCC	GGCACGGTGG	AAGCCGGGA	CATCATGATG	360
GTCGGCACC	ACTTCTACAT	CGGCGAATCG	GCCCGCACCA	ACGCCGAGGG	CGCCCGGCAG	420
ATGATCGCGA	TCTTGGAGAA	ACATGGCTCG	AGGGGCTCG	TGGTCCGCCT	GGAAAAGGTC	480
CTGACCTGA	AGACCGGGCT	CGCCTACCTG	GAACACAACA	ACCTGCTGGC	CGCCGGCGAG	540
TTCGTAGCA	AGCCGGAGTT	CCAGGACTTC	AACATCATCG	AGATCCCCGA	AGAGGAGTCC	600
TACGCCGCCA	ACTGCATCTG	GGTCAACGAA	AGGGTGATCA	TGCCCCCGGG	CTATCCCCGG	660
ACCCCGAGA	AGATGCCCG	CCTCGGCTAC	CGGGTGATCG	AGGTGGACAC	CTCCGAATAT	720
CGCAAGATCG	ACGGCGGCGT	CAGTTGCATG	TCGCTGGCCT	TCTGA		765

(2) INFORMATION FOR SEQ ID NO: 8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Phe	Lys	His	Ile	Ile	Ala	Arg	Thr	Pro	Ala	Arg	Ser	Leu	Val	Asp
1				5				10						15	
Gly	Leu	Thr	Ser	Ser	His	Leu	Gly	Lys	Pro	Asp	Tyr	Ala	Lys	Ala	Leu
					20			25						30	
Glu	Gln	His	Asn	Ala	Tyr	Ile	Arg	Ala	Leu	Gln	Thr	Cys	Asp	Val	Asp
					35			40						45	
Ile	Thr	Leu	Leu	Pro	Pro	Asp	Glu	Arg	Phe	Pro	Asp	Ser	Val	Phe	Val
				50				55						60	
Glu	Asp	Pro	Val	Leu	Cys	Thr	Ser	Arg	Cys	Ala	Ile	Ile	Thr	Arg	Pro
				65				70						80	

.9.

Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val
85 90 95

Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
100 105 110

Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
115 120 125

Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
130 135 140

Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
145 150 155 160

Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu
165 170 175

Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile
180 185 190

Ile Glu Ile Pro Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
195 200 205

Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys
210 215 220

Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr
225 230 235 240

Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe
245 250

(2) INFORMATION FOR SEQ ID NO: 9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGG AAAAAACCAA ACTTGGCGTC CACTCCGAAG CGGGCAAACT GCGCAAAGTG 60
ATGGTCTCT CGCCCCGACT CGCCCACCAAG CGCCTGACCC CGAGCAACTG CGACGAGTTG 120
CTGTTCGACG ACGTGATCTG GGTGAACCAAG GCCAAGCGCG ACCACTTCGA CTTCGTCACC 180

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AAGATGCGCG AGOGCGGCAT CGACGTCCTC GAGATGACA ATCTGCTGAC CGAGACCAC	240
CAGAACCCGG AAGCGCTGAA GTGGATCCTC GATCGCAAGA TCACCCCGA CAGCGTCGGC	300
CTGGCCCTGA CCAGCGAGCT CGCGCTCTGG CTGGAGAGCC TGGAGCCGCG CAAGCTGGCC	360
GAGTACCTGA TCGGCCGGGT CGCCGCTGAC GACCTGCCCG CAGCGAAGG CGCCAACATC	420
CTCAAGATGT ACCGCGAGTA CCTGGCCAT TCCAGCTTCC TGCTGCCGCC GTTGCCGAAC	480
ACCCAGTTCA CCCCGCACAC CACTTGCTGG ATCTACGGG GCGTGACCT GAACCGATG	540
TACTGGCCGG CGCGACGACA GGAAACCTG CTGACCAACG CCACTACAA GTTCCACCCC	600
GAGTTGCCA ACGCCGAGTT CGAGATCTGG TACGGCGACC CGGACAAGGA CCACGGCTCC	660
TCGACCCCTGG AAGGCCGGCGA CGTGTGATGCCG ATCGGCAACG GCGTGGTCCT GATCGGCATG	720
GGCGAGCGCT CCTCGCCCA GCCCATCGGT CAGGTCGCCG AGTCGCTGTT CGCCAAAGGGC	780
GCGCCGAGC GGGTGTGCGT CGCCGGCCTG CCGAAGTCGG GCGCCGCGAT GCACCTGGAC	840
ACCGTGTTCGA GCTTCTGCCA CGCGCACCTG GTCAACGGTCT TCCCGGAAGT GGTCAAGGAA	900
ATCGTCCCT TCAGGCTCGG CCCCAGATCGG AGCAGCCCC ACAGCATGAA CATCGCCGC	960
GAGGAGAAA CCTTCTCTGA AGTGGTCGCC GAATCCCTCG GCTGAAAGAA ACTGGCGCTG	1020
GTCGAGACCG GCGGCAACAG CTTCGCCGCC GAGCGCGASC AATGGGACGA CGGTAACAAC	1080
GTGGTCTGCC TGGAGCCGGG CGTGGTGGTC GGCTACGACG GCAACACCTA CACCAACACC	1140
CTGCTGCGCA AGGCCGGCGT CGAGGTCATC ACCATCAGGG CCAGCGAACT GGGTGGCGGT	1200
CGCGGCGGGG GCGACTGCAT GACCTGCCCG ATCGTCCCGG ACCCGATGAA CTACTGA	1257

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Ser	Thr	Glu	Lys	Thr	Lys	Leu	Gly	Val	His	Ser	Glu	Ala	Gly	Lys
1					5				10		15				

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Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
20 25 30

Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
35 40 45

Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
50 55 60

Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
65 70 75 80

Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala
85 90 95

Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
100 105 110

Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala
115 120 125

Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr
130 135 140

Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn
145 150 155 160

Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
165 170 175

Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
180 185 190

Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
195 200 205

Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu
210 215 220

Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met
225 230 235 240

Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu
245 250 255

Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys
260 265 270

Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
275 280 285

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Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe
290 295 300

Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
305 310 315 320

Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys
325 330 335

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
340 345 350

Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
355 360 365

Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
370 375 380

Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly
385 390 395 400

Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile
405 410 415

Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i1) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGTATCAAT GGAAATAGG CAACGACCAT CGTTTGATTG TGAAATCAGA GCCAAATATC	60
GTGGTTTAT GACGGATTCC TACGTCGCTG CTGCCCGTCT AGGGTCACCT GCACGCCGCA	120
CCCCCGGGAC GCGGCCTAT GCAATGACCC CGCCGGCTT CTTTGCCTGC GCATACGCGA	180
TCAACCCCTG GATGGACGTC ACCGGCCAG TCGACGCTCA AGTCGGCAA GCACAGTGG	240
AGCACCTCCA CCAGACCTAT CTTCGGCTAG GCCACAGCGT GGATCTGATC GAGCCCATT	300
CCGGGTTACC GGACATGGTG TACACGGCA ACGGTGGTT CATCGCGCAC GACATCGCG	360

TGGTCCCGG	GTTCCGGTTC	CCCGAACGAG	CTGGTGAGTC	TAGAGCTAT	GCCAGCTGGA	420
TGTCCTCGGT	CGGATATCGC	CGGGTGACCA	CCCACCGT	CAACGAGGGA	CAGGGCGACC	480
TGCTGATGGT	TGGGAAAGG	GTGTTGGCGG	GCTACGGCTT	TCCACAGAC	CAGGGCGCAC	540
ACGCCGAAAT	CGCCGCGGTG	CTTGGCTGTC	CGGTGGCTC	CCTCGAGTTG	GTCGACCCAC	600
GGTTCTATCA	CCTGGACACC	GCCTGGCCG	TGCTCGACGA	CCACACGATE	GCCTACTACC	660
CGCCGGCGTT	CACTACGGCA	GCGCAGGAAC	AGTTGTGCGG	GCTGTTCCCC	GACGGATTG	720
TGGTCGGCAG	TGCCGAGCG	TTCGTTTCG	GACTCAACCC	CGTCTCTGAC	GCTCTGAACG	780
TAGTGCTTCC	GGTGGCGGCC	ATGGGTTTG	CGGCGCAGTT	ACGCGCAGCC	GGCTTCGAGC	840
CGGTGCGTGT	CGATCTGTCC	GAGCTGCTCA	AGGGCGGCGG	TTCCGTCAG	TGCTGCAEGC	900
TGGAGATACA	CCCATGACAA	ATCTCGCGA	TGCCACTCAAG	GCCACTATGG	CACTGGTCCA	960
AAGGCATGCA	GCGCACAAATT	ATTCGCCGCT	GCCTGTGGTG	GCGGCCAGCG	CTGA	1014

(2) INFORMATION FOR SEQ ID NO: 12:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Asn	Val	Ser	Met	Glu	Asn	Thr	Gln	Arg	Pro	Ser	Phe	Asp	Cys	Glu	Ile
1				5				10					15		
Arg	Ala	Lys	Tyr	Arg	Trp	Phe	Met	Thr	Asp	Ser	Tyr	Val	Ala	Ala	Ala
				20			25					30			
Arg	Leu	Gly	Ser	Pro	Ala	Arg	Arg	Thr	Pro	Arg	Thr	Arg	Arg	Tyr	Ala
	35				40			45							
Met	Thr	Pro	Pro	Ala	Phe	Phe	Ala	Val	Ala	Tyr	Ala	Ile	Asn	Pro	Trp
	50				55			60							
Met	Asp	Val	Thr	Ala	Pro	Val	Asp	Val	Gln	Val	Ala	Gln	Ala	Gln	Trp
	65				70			75				80			
Glu	His	Leu	His	Gln	Thr	Tyr	Leu	Arg	Leu	Gly	His	Ser	Val	Asp	Leu
					85			90				95			

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Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gin Gly Asp
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu
275 280 285

Leu Leu Lys Gly Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His
290 295 300

Pro
305